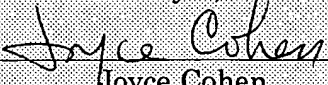




Patent Docket P0871P4D2

THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of Dan L. Eaton et al. Serial No.: 08/423,194 Filed: 18 April 1995 For: MPL LIGAND	Group Art Unit: 1812 Examiner: L. Spector <div style="border: 1px solid black; padding: 5px;"><p style="text-align: center; margin: 0;">CERTIFICATE OF MAILING</p><p style="font-size: small; margin: 0;">I hereby certify that this correspondence is being deposited with the United States Postal Service with sufficient postage as first class mail in an envelope addressed to: Assistant Commissioner of Patents, Washington, D.C. 20231 on</p><p style="text-align: center; margin: 5px 0;">January 2, 1997</p><p style="text-align: center; margin: 0;"> Joyce Cohen</p></div>
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CERTIFICATE RE: SEQUENCE LISTING

RESPONSE UNDER 37 CFR § 1.821(f) and (g)

Assistant Commissioner of Patents
Washington, D.C. 20231

Sir:

I hereby state that the Sequence Listing submitted herewith is submitted in paper copy and a computer-readable diskette, and that the content of the paper and computer readable copies are the same. I further state that this submission includes no new matter.

Respectfully submitted,

GENENTECH, INC.

Date: January 2, 1997

By: 

Daryl B. Winter
Reg. No. 32,637

460 Pt. San Bruno Blvd.
So. San Francisco, CA 94080-4990
Phone: (415) 225-1249
Fax: (415) 952-9881

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).

☒ 7. Seq ID5 is Reversed polarity
Other: _____

Applicant must provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call (703) 308-1123

For CRF submission help, call (703) 308-4212

For PatentIn software help, call (703) 557-0400

Please return a copy of this notice with your response.



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Eaton, Dan L.
de Sauvage, Frederic J.
- (ii) TITLE OF INVENTION: MPL LIGAND
- 10 (iii) NUMBER OF SEQUENCES: 77
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 460 Point San Bruno Blvd
15 (C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080
- 20 (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: patin (Genentech)
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/423194
(B) FILING DATE: 18-APR-1995
(C) CLASSIFICATION:
- 30 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/249376
(B) FILING DATE: 25-MAY-1994
- 35 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/223263
(B) FILING DATE: 04-APR-1994
- 40 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/196689
(B) FILING DATE: 15-FEB-1994
- 45 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/185607
(B) FILING DATE: 21-JAN-1994
- 50 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/176553
(B) FILING DATE: 03-JAN-1994
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Winter, Daryl B.

(B) REGISTRATION NUMBER: 32,637
(C) REFERENCE/DOCKET NUMBER: 871P4D2

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415/225-1249
(B) TELEFAX: 415/952-9881
(C) TELEX: 910/371-7168

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 353 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr
-21 -20 -15 -10
Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu
-5 1 5
Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser
10 15 20
Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val
25 30 35
Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln
40 45 50
Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu
55 60 65
Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr
70 75 80
Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu
85 90 95
Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro
100 105 110
Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu
115 120 125
Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu
130 135 140
Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr Thr
145 150 155

Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu Asn Glu Leu
160 165 170

5 Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr Ala Ser
175 180 185

Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly Phe
190 195 200

10 Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu
205 210 215

Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn
220 225 230

15 Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr Leu Gly
235 240 245

Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser Leu Pro
250 255 260

20 Pro Asn Leu Gln Pro Gly Tyr Ser Pro Ser Pro Thr His Pro Pro
265 270 275

25 Thr Gly Gln Tyr Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro Thr
280 285 290

Pro Val Val Gln Leu His Pro Leu Leu Pro Asp Pro Ser Ala Pro
295 300 305

30 Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His
310 315 320

Bl cont
35 Ser Gln Asn Leu Ser Gln Glu Gly
325 330 332

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1795 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TCTTCCTACC CATCTGCTCC CCAGAGGGCT GCCTGCTGTG CACTTGGGTC 50

CTGGAGCCCT TCTCCACCCG GATAGATTCC TCACCCTTGG CCCGCCTTTG 100

CCCCACCCTA CTCTGCCCAG AAGTGCAAGA GCCTAAGCCG CCTCCATGGC 150
 CCCAGGAAGG ATTCAGGGGA GAGGCCCCAA ACAGGGAGCC ACGCCAGCCA 200
 GACACCCCGG CCAGAATGGA GCTGACTGAA TTGCTCCTCG TGGTCATGCT 250
 TCTCCTAACT GCAAGGCTAA CGCTGTCCAG CCCGGCTCCT CCTGCTTGTG 300
 ACCTCCGAGT CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC 350
 AGACTGAGCC AGTGCCCAGA GGTTCACCCT TTGCCTACAC CTGTCCTGCT 400
 GCCTGCTGTG GACTTTAGCT TGGGAGAATG GAAAACCCAG ATGGAGGAGA 450
 CCAAGGCACA GGACATTCTG GGAGCAGTGA CCCTTCTGCT GGAGGGAGTG 500
 ATGGCAGCAC GGGGACAACT GGGACCCACT TGCCTCTCAT CCCTCCTGGG 550
 GCAGCTTTCT GGACAGGTCC GTCTCCTCCT TGGGGCCCTG CAGAGCCTCC 600
 TTGGAACCCA GCTTCCTCCA CAGGGCAGGA CCACAGCTCA CAAGGATCCC 650
 AATGCCATCT TCCTGAGCTT CCAACACCTG CTCCGAGGAA AGGTGCGTTT 700
 CCTGATGCTT GTAGGAGGGT CCACCCTCTG CGTCAGGCGG GCCCCACCCA 750
 CCACAGCTGT CCCCAGCAGA ACCTCTCTAG TCCTCACACT GAACGAGCTC 800
 CCAAACAGGA CTTCTGGATT GTTGAGAGACA AACTTCACTG CCTCAGCCAG 850
 AACTACTGGC TCTGGGCTTC TGAAGTGGCA GCAGGGATTC AGAGCCAAGA 900
 TTCCTGGTCT GCTGAACCAA ACCTCCAGGT CCCTGGACCA AATCCCCGGA 950
 TACCTGAACA GGATACACGA ACTCTTGAAT GGAATCTGTG GACTCTTTCC 1000

TGGACCCTCA CGCAGGACCC TAGGAGCCCC GGACATTTC TCAGGAACAT 1050

5 CAGACACAGG CTCCCTGCCA CCCAACCTCC AGCCTGGATA TTCTCCTTCC 1100

CCAACCCATC CTCCTACTGG ACAGTATACG CTCTTCCCTC TTCCACCCAC 1150

10 CTTGCCCACC CCTGTGGTCC AGCTCCACCC CCTGCTTCCT GACCCTTCTG 1200

CTCCAACGCC CACCCCTACC AGCCCTCTTC TAAACACATC CTACACCCAC 1250

15 TCCCAGAATC TGTCTCAGGA AGGGTAAGGT TCTCAGACAC TGCCGACATC 1300

20 AGCATTGTCT CATGTACAGC TCCCTTCCCT GCAGGGCGCC CCTGGGAGAC 1350

AACTGGACAA GATTTCCTAC TTTCTCCTGA AACCCAAAGC CCTGGTAAAA 1400

25 GGGATACACA GGA CTGAAAA GGAATCATT TTCACTGTA CATTATAAAC 1450

CTTCAGAAGC TATTTTTTTA AGCTATCAGC AATACTCATC AGAGCAGCTA 1500

30 GCTCTTTGGT CTATTTTCTG CAGAAATTG CAACTCACTG ATTCTCTACA 1550

35 TGCTCTTTTT CTGTGATAAC TCTGCAAAGG CCTGGGCTGG CCTGGCAGTT 1600

GAACAGAGGG AGAGACTAAC CTTGAGTCAG AAAACAGAGA AAGGGTAATT 1650

40 TCCTTTGCTT CAAATTCAAG GCCTTCCAAC GCCCCCATCC CCTTTACTAT 1700

CATTCTCAGT GGGACTCTGA TCCCATATTC TTAACAGATC TTTACTCTTG 1750

45 AGAAATGAAT AAGCTTTCTC TCAGAAAAAA AAAAAAAAAA AAAAA 1795

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Leu Leu Leu Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu
-16 -15 -10 -5
Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys
1 5 10
Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu
15 20 25 26

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 390 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTCCTGG AATACCAGCT GACAATGATT TCCTCCTCAT CTTTCAACCT 50
CACCTCTCCT CATCTAAGAA TTGCTCCTCG TGGTCATGCT TCTCCTAACT 100
GCAAGGCTAA CGCTGTCCAG CCCGGCTCCT CCTGCTTGTG ACCTCCGAGT 150
CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC AGACTGGTGA 200
GAACTCCCAA CATTATCCCC TTTATCCGCG TAACTGGTAA GACACCCATA 250
CTCCCAGGAA GACACCATCA CTTCTCTTAA CTCCTTGACC CAATGACTAT 300
TCTTCCCATA TTGTCCCCAC CTA CTGATCA CACTCTCTGA CAAGAATTAT 350
TCTTCACAAT ACAGCCCGCA TTAAAAGCT CTCGTCTAGA 390

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCTAGACGAG AGCTTTTAAA TCGGGCTGT ATTGTGAAGA ATAATTCTTG 50
TCAGAGAGTG TGATCAGTAG GTGGGGACAA TATGGGAAGA ATAGTCATTG 100
GGTCAAGGAG TTAGAGGAAG TGATGGTGTC TTCCTGGGAG TATGGGTGTC 150
TTACCAGTTA CGCGGATAAA GGGGATAATG TTGGGAGTTC TCACCAGTCT 200
GCTGTGAAGG ACATGGGAGT CACGAAGCAG TTTACTGAGG ACTCGGAGGT 250
CACAAGCAGG AGGAGCCGGG CTGGACAGCG TTAGCCTTGC AGTTAGGAGA 300
AGCATGACCA CGAGGAGCAA TTCTTAGATG AGGAGAGGTG AGGTTGAAAG 350
ATGAGGAGGA AATCATTGTC AGCTGGTATT CCAGGAATTC 390

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu
1 5 10 15
Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro
20 25 30
Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp
35 40 45
Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala
50 55 60
Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met
65 70 75

	Ala	Ala	Arg	Gly	Gln 80	Leu	Gly	Pro	Thr	Cys 85	Leu	Ser	Ser	Leu	Leu 90
5	Gly	Gln	Leu	Ser	Gly 95	Gln	Val	Arg	Leu	Leu 100	Leu	Gly	Ala	Leu	Gln 105
	Ser	Leu	Leu	Gly	Thr 110	Gln	Leu	Pro	Pro	Gln 115	Gly	Arg	Thr	Thr	Ala 120
10	His	Lys	Asp	Pro	Asn 125	Ala	Ile	Phe	Leu	Ser 130	Phe	Gln	His	Leu	Leu 135
	Arg	Gly	Lys	Val	Arg 140	Phe	Leu	Met	Leu	Val 145	Gly	Gly	Ser	Thr	Leu 150
15	Cys	Val	Arg	Arg	Ala 155	Pro	Pro	Thr	Thr	Ala 160	Val	Pro	Ser	Arg	Thr 165
20	Ser	Leu	Val	Leu	Thr 170	Leu	Asn	Glu	Leu	Pro 175	Asn	Arg	Thr	Ser	Gly 180
	Leu	Leu	Glu	Thr	Asn 185	Phe	Thr	Ala	Ser	Ala 190	Arg	Thr	Thr	Gly	Ser 195
25	Gly	Leu	Leu	Lys	Trp 200	Gln	Gln	Gly	Phe	Arg 205	Ala	Lys	Ile	Pro	Gly 210
	Leu	Leu	Asn	Gln	Thr 215	Ser	Arg	Ser	Leu	Asp 220	Gln	Ile	Pro	Gly	Tyr 225
30	Leu	Asn	Arg	Ile	His 230	Glu	Leu	Leu	Asn	Gly 235	Thr	Arg	Gly	Leu	Phe 240
<i>B1</i> <i>Cont</i> 35	Pro	Gly	Pro	Ser	Arg 245	Arg	Thr	Leu	Gly	Ala 250	Pro	Asp	Ile	Ser	Ser 255
	Gly	Thr	Ser	Asp	Thr 260	Gly	Ser	Leu	Pro	Pro 265	Asn	Leu	Gln	Pro	Gly 270
40	Tyr	Ser	Pro	Ser	Pro 275	Thr	His	Pro	Pro	Thr 280	Gly	Gln	Tyr	Thr	Leu 285
	Phe	Pro	Leu	Pro	Pro 290	Thr	Leu	Pro	Thr	Pro 295	Val	Val	Gln	Leu	His 300
45	Pro	Leu	Leu	Pro	Asp 305	Pro	Ser	Ala	Pro	Thr 310	Pro	Thr	Pro	Thr	Ser 315
50	Pro	Leu	Leu	Asn	Thr 320	Ser	Tyr	Thr	His	Ser 325	Gln	Asn	Leu	Ser	Gln 330

Glu Gly
332

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr
1 5 10 15
Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala
20 25 30
Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys
35 40 45
Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala
50 55 60
Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu
65 70 75
Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro
80 85 90
Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu
95 100 105
Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser
110 115 120
Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala
125 130 135
Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg
140 145 150
Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
155 160 165
Arg
166

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 328 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

	Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	Lys	Leu	1	5	10	15
10	Leu	Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro	20	25	30	
	Glu	Val	His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	35	40	45	
15	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	50	55	60	
20	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	65	70	75	
	Ala	Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	80	85	90	
25	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	95	100	105	
30	Ser	Leu	Leu	Gly	Thr	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	110	115	120	
	Asn	Ala	Ile	Phe	Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	125	130	135	
35	Arg	Phe	Leu	Met	Leu	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Arg	140	145	150	
<i>B1</i> <i>Cont</i>	Ala	Pro	Pro	Thr	Thr	Ala	Val	Pro	Ser	Arg	Thr	Ser	Leu	Val	Leu	155	160	165	
40	Thr	Leu	Asn	Glu	Leu	Pro	Asn	Arg	Thr	Ser	Gly	Leu	Leu	Glu	Thr	170	175	180	
45	Asn	Phe	Thr	Ala	Ser	Ala	Arg	Thr	Thr	Gly	Ser	Gly	Leu	Leu	Lys	185	190	195	
	Trp	Gln	Gln	Gly	Phe	Arg	Ala	Lys	Ile	Pro	Gly	Leu	Leu	Asn	Gln	200	205	210	
50	Thr	Ser	Arg	Ser	Leu	Asp	Gln	Ile	Pro	Gly	Tyr	Leu	Asn	Arg	Ile	215	220	225	

	His	Glu	Leu	Leu	Asn	Gly	Thr	Arg	Gly	Leu	Phe	Pro	Gly	Pro	Ser	
					230					235					240	
5	Arg	Arg	Thr	Leu	Gly	Ala	Pro	Asp	Ile	Ser	Ser	Gly	Thr	Ser	Asp	
					245					250					255	
	Thr	Gly	Ser	Leu	Pro	Pro	Asn	Leu	Gln	Pro	Gly	Tyr	Ser	Pro	Ser	
					260					265					270	
10	Pro	Thr	His	Pro	Pro	Thr	Gly	Gln	Tyr	Thr	Leu	Phe	Pro	Leu	Pro	
					275					280					285	
	Pro	Thr	Leu	Pro	Thr	Pro	Val	Val	Gln	Leu	His	Pro	Leu	Leu	Pro	
15					290					295					300	
	Asp	Pro	Ser	Ala	Pro	Thr	Pro	Thr	Pro	Thr	Ser	Pro	Leu	Leu	Asn	
					305					310					315	
20	Thr	Ser	Tyr	Thr	His	Ser	Gln	Asn	Leu	Ser	Gln	Glu	Gly			
					320					325			328			

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

30	Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	Lys	Leu	
	1				5					10					15	
35	Leu	Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro	
					20					25					30	
	Glu	Val	His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	
					35					40					45	
40	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	
					50					55					60	
45	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	
					65					70					75	
	Ala	Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	
					80					85					90	
50	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	
					95					100					105	

	Ser	Leu	Leu	Gly	Thr	Gln	Leu	Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	
					110					115					120	
5	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	Leu	Ser	Phe	Gln	His	Leu	Leu	
					125					130					135	
	Arg	Gly	Lys	Asp	Phe	Trp	Ile	Val	Gly	Asp	Lys	Leu	His	Cys	Leu	
					140					145					150	
10	Ser	Gln	Asn	Tyr	Trp	Leu	Trp	Ala	Ser	Glu	Val	Ala	Ala	Gly	Ile	
					155					160					165	
	Gln	Ser	Gln	Asp	Ser	Trp	Ser	Ala	Glu	Pro	Asn	Leu	Gln	Val	Pro	
					170					175					180	
15	Gly	Pro	Asn	Pro	Arg	Ile	Pro	Glu	Gln	Asp	Thr	Arg	Thr	Leu	Glu	
					185					190					195	
	Trp	Asn	Ser	Trp	Thr	Leu	Ser	Trp	Thr	Leu	Thr	Gln	Asp	Pro	Arg	
20					200					205					210	
	Ser	Pro	Gly	His	Phe	Leu	Arg	Asn	Ile	Arg	His	Arg	Leu	Pro	Ala	
					215					220					225	
25	Thr	Gln	Pro	Pro	Ala	Trp	Ile	Phe	Ser	Phe	Pro	Asn	Pro	Ser	Ser	
					230					235					240	
	Tyr	Trp	Thr	Val	Tyr	Ala	Leu	Pro	Ser	Ser	Thr	His	Leu	Ala	His	
					245					250					255	
30	Pro	Cys	Gly	Pro	Ala	Pro	Pro	Pro	Ala	Ser						
					260					265						

B! cont
35 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

45	Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	Lys	Leu	
	1				5					10					15	
	Leu	Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro	
					20					25					30	
50	Glu	Val	His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	
					35					40					45	

	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	
					50					55					60	
5	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	
					65					70					75	
	Ala	Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	
					80					85					90	
10	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	
					95					100					105	
	Ser	Leu	Leu	Gly	Thr	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	
					110					115					120	
15	Asn	Ala	Ile	Phe	Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Asp	
					125					130					135	
20	Phe	Trp	Ile	Val	Gly	Asp	Lys	Leu	His	Cys	Leu	Ser	Gln	Asn	Tyr	
					140					145					150	
	Trp	Leu	Trp	Ala	Ser	Glu	Val	Ala	Ala	Gly	Ile	Gln	Ser	Gln	Asp	
					155					160					165	
25	Ser	Trp	Ser	Ala	Glu	Pro	Asn	Leu	Gln	Val	Pro	Gly	Pro	Asn	Pro	
					170					175					180	
	Arg	Ile	Pro	Glu	Gln	Asp	Thr	Arg	Thr	Leu	Glu	Trp	Asn	Ser	Trp	
					185					190					195	
30	Thr	Leu	Ser	Trp	Thr	Leu	Thr	Gln	Asp	Pro	Arg	Ser	Pro	Gly	His	
					200					205					210	
	Phe	Leu	Arg	Asn	Ile	Arg	His	Arg	Leu	Pro	Ala	Thr	Gln	Pro	Pro	
					215					220					225	
35	Ala	Trp	Ile	Phe	Ser	Phe	Pro	Asn	Pro	Ser	Ser	Tyr	Trp	Thr	Val	
					230					235					240	
40	Tyr	Ala	Leu	Pro	Ser	Ser	Thr	His	Leu	Ala	His	Pro	Cys	Gly	Pro	
					245					250					255	
45	Ala	Pro	Pro	Pro	Ala	Ser										
					260	261										

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1443 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

5 GAGTCCTTGG CCCACCTCTC TCCCACCCGA CTCTGCCGAA AGAAGCACAG 50
AAGCTCAAGC CGCCTCCATG GCCCCAGGAA AGATTCAGGG GAGAGGCCCC 100
10 ATACAGGGAG CCACTTCAGT TAGACACCCT GGCCAGAATG GAGCTGACTG 150
ATTGCTCCT GCGGGCCATG CTTCTTGAG TGGCAAGACT AACTCTGTCC 200
AGCCCCGTAG CTCCTGCCTG TGACCCCAAG CTCCTAAATA AACTGCTGCG 250
20 TGAATCCAC CTCCTTCACA GCGACTGAG TCAGTGTCCC GACGTCGACC 300
CTTTGTCTAT CCCTGTTCTG CTGCCTGCTG TGGACTTTAG CCTGGGAGAA 350
25 TGGAAAACCC AGACGGAACA GAGCAAGGCA CAGGACATTC TAGGGGCAGT 400
GTCCCTTCTA CTGGAGGGAG TGATGGCAGC ACGAGGACAG TTGGAACCCT 450
CCTGCCTCTC ATCCCTCCTG GGACAGCTTT CTGGGCAGGT TCGCCTCCTC 500
35 TTGGGGGCCC TGCAGGGCCT CCTAGGAACC CAGGGCAGGA CCACAGCTCA 550
CAAGGACCCC AATGCCCTCT TCTTGAGCTT GCAACAACCTG CTTGCGGGAA 600
40 AGGTGCGCTT CCTGCTTCTG GTAGAAGGTC CCACCCTCTG TGTCAGACGG 650
ACCCTGCCAA CCACAGCTGT CCAAGCAGT ACTTCTCAAC TCCTCACACT 700
AAACAAGTTC CCAAACAGGA CTTCTGGATT GTTGGAGACG AACTTCAGTG 750
50 TCACAGCCAG AACTGCTGGC CCTGGACTTC TGAGCAGGCT TCAGGGATTC 800

AGAGTCAAGA TTACTCCTGG TCAGCTAAAT CAAACCTCCA GGTCCCCAGT 850
 CCAAATCTCT GGATACCTGA ACAGGACACA CGGACCTGTG AATGGAACTC 900
 ATGGGCTCTT TGCTGGAACC TCACTTCAGA CCCTGGAAGC CTCAGACATC 950
 TCGCCCGGAG CTTTCAACAA AGGCTCCCTG GCATTCAACC TCCAGGGTGG 1000
 ACTTCCTCCT TCTCCAAGCC TTGCTCCTGA TGGACACACA CCCTTCCCTC 1050
 CTTACCTGC CTTGCCCACC ACCCATGGAT CTCCACCCCA GCTCCACCCC 1100
 CTGTTTCCTG ACCCTTCCAC CACCATGCCT AACTCTACCG CCCCTCATCC 1150
 AGTCACAATG TACCCTCATC CCAGGAATTT GTCTCAGGAA ACATAGCGCG 1200
 GGCCTGGCC CAGTGAGCGT CTGCAGCTTC TCTCGGGGAC AAGCTTCCCC 1250
 AGGAAGGCTG AGAGGCAGCT GCATCTGCTC CAGATGTTCT GCTTTCACCT 1300
 AAAAGGCCCT GGGGAAGGGA TACACAGCAC TGGAGATTGT AAAATTTTAG 1350
 GAGCTATTTT TTTTAACT ATCAGCAATA TTCATCAGAG CAGCTAGCGA 1400
 TCTTTGGTCT ATTTTCGGTA TAAATTGAA AATCACTAAT TCT 1443

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Glu Leu Thr Asp Leu Leu Leu Ala Ala Met Leu Leu Ala Val
 -21 -20 -15 -10

	Ala	Arg	Leu	Thr	Leu	Ser	Ser	Pro	Val	Ala	Pro	Ala	Cys	Asp	Pro
	-5						1				5				
5	Arg	Leu	Leu	Asn	Lys	Leu	Leu	Arg	Asp	Ser	His	Leu	Leu	His	Ser
	10					15					20				
	Arg	Leu	Ser	Gln	Cys	Pro	Asp	Val	Asp	Pro	Leu	Ser	Ile	Pro	Val
	25					30					35				
10	Leu	Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln
	40					45					50				
	Thr	Glu	Gln	Ser	Lys	Ala	Gln	Asp	Ile	Leu	Gly	Ala	Val	Ser	Leu
	55					60					65				
15	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly	Gln	Leu	Glu	Pro	Ser
	70					75					80				
	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu
20	85					90					95				
	Leu	Leu	Gly	Ala	Leu	Gln	Gly	Leu	Leu	Gly	Thr	Gln	Gly	Arg	Thr
	100					105					110				
25	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Leu	Phe	Leu	Ser	Leu	Gln	Gln
	115					120					125				
	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Leu	Leu	Val	Glu	Gly	Pro
	130					135					140				
30	Thr	Leu	Cys	Val	Arg	Arg	Thr	Leu	Pro	Thr	Thr	Ala	Val	Pro	Ser
	145					150					155				
	Ser	Thr	Ser	Gln	Leu	Leu	Thr	Leu	Asn	Lys	Phe	Pro	Asn	Arg	Thr
35	160					165					170				
	Ser	Gly	Leu	Leu	Glu	Thr	Asn	Phe	Ser	Val	Thr	Ala	Arg	Thr	Ala
	175					180					185				
40	Gly	Pro	Gly	Leu	Leu	Ser	Arg	Leu	Gln	Gly	Phe	Arg	Val	Lys	Ile
	190					195					200				
	Thr	Pro	Gly	Gln	Leu	Asn	Gln	Thr	Ser	Arg	Ser	Pro	Val	Gln	Ile
45	205					210					215				
	Ser	Gly	Tyr	Leu	Asn	Arg	Thr	His	Gly	Pro	Val	Asn	Gly	Thr	His
	220					225					230				
50	Gly	Leu	Phe	Ala	Gly	Thr	Ser	Leu	Gln	Thr	Leu	Glu	Ala	Ser	Asp
	235					240					245				

Ile Ser Pro Gly Ala Phe Asn Lys Gly Ser Leu Ala Phe Asn Leu
250 255 260

Gln Gly Gly Leu Pro Pro Ser Pro Ser Leu Ala Pro Asp Gly His
265 270 275

Thr Pro Phe Pro Pro Ser Pro Ala Leu Pro Thr Thr His Gly Ser
280 285 290

Pro Pro Gln Leu His Pro Leu Phe Pro Asp Pro Ser Thr Thr Met
295 300 305

Pro Asn Ser Thr Ala Pro His Pro Val Thr Met Tyr Pro His Pro
310 315 320

Arg Asn Leu Ser Gln Glu Thr
325 330 331

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1536 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGTCCTTGG CCCACCTCTC TCCCACCCGA CTCTGCCGAA AGAAGCACAG 50

AAGCTCAAGC CGCCTCCATG GCCCCAGGAA AGATTCAGGG GAGAGGCCCC 100

ATACAGGGAG CCACTTCAGT TAGACACCCT GGCCAGAATG GAGCTGACTG 150

ATTGCTCCT GCGGCCCATG CTTCTTGCA GGGCAAGACT AACTCTGTCC 200

AGCCCCGTAG CTCCTGCCTG TGACCCCA GATCCTAAATA AACTGCTGCG 250

TGACTCCCAC CTCCTTCACA GCCGACTGAG TCAGTGTCCC GACGTCGACC 300

CTTTGTCTAT CCCTGTTCTG CTGCCTGCTG TGGACTTTAG CCTGGGAGAA 350

TGAAAACCC AGACGGAACA GAGCAAGGCA CAGGACATTC TAGGGGCAGT 400

GTCCCTTCTA CTGGAGGGAG TGATGGCAGC ACGAGGACAG TTGGAACCCT 450
 CCTGCCTCTC ATCCCTCCTG GGACAGCTTT CTGGGCAGGT TCGCCTCCTC 500
 TTGGGGGCCC TGCAGGGCCT CCTAGGAACC CAGCTTCCTC TACAGGGCAG 550
 GACCACAGCT CACAAGGACC CCAATGCCCT CTTCTTGAGC TTGCAACAAC 600
 TGCTTCGGGG AAAGGTGCGC TTCCTGCTTC TGGTAGAAGG TCCCACCCTC 650
 TGTGTCAGAC GGACCCTGCC AACCACAGCT GTCCCAAGCA GTACTTCTCA 700
 ACTCCTCACA CTAAACAAGT TCCCAAACAG GACTTCTGGA TTGTTGGAGA 750
 CGAACTTCAG TGTCACAGCC AGAACTGCTG GCCCTGGACT TCTGAGCAGG 800
 CTTCAGGGAT TCAGAGTCAA GATTACTCCT GGTCAGCTAA ATCAAACCTC 850
 CAGGTCCCCA GTCCAAATCT CTGGATACCT GAACAGGACA CACGGACCTG 900
 TGAATGGAAC TCATGGGCTC TTTGCTGGAA CCTCACTTCA GACCCTGGAA 950
 GCCTCAGACA TCTCGCCCGG AGCTTTCAAC AAAGGCTCCC TGGCATTCAA 1000
 CCTCCAGGGT GGACTTCCTC CTTCTCCAAG CCTTGCTCCT GATGGACACA 1050
 CACCCTTCCC TCCTTCACCT GCCTTGCCCA CCACCCATGG ATCTCCACCC 1100
 CAGCTCCACC CCCTGTTTCC TGACCCTTCC ACCACCATGC CTAACTCTAC 1150
 CGCCCCTCAT CCAGTCACAA TGTACCCTCA TCCCAGGAAT TTGTCTCAGG 1200
 AACATAGCG CGGGCACTGG CCCAGTGAGC GTCTGCAGCT TCTCTCGGGG 1250
 ACAAGCTTCC CCAGGAAGGC TGAGAGGCAG CTGCATCTGC TCCAGATGTT 1300

CTGCTTTCAC CTAAAAGGCC CTGGGGAAGG GATACACAGC ACTGGAGATT 1350

5 GTAAAATTTT AGGAGCTATT TTTTTTTAAC CTATCAGCAA TATTCATCAG 1400

AGCAGCTAGC GATCTTTGGT CTATTTTCGG TATAAATTG AAAATCACTA 1450

10 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1500

15 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA 1536

(2) INFORMATION FOR SEQ ID NO:14:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 356 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Glu Leu Thr Asp Leu Leu Leu Ala Ala Met Leu Leu Ala Val
-21 -20 -15 -10

30 Ala Arg Leu Thr Leu Ser Ser Pro Val Ala Pro Ala Cys Asp Pro
-5 1 5

Arg Leu Leu Asn Lys Leu Leu Arg Asp Ser His Leu Leu His Ser
10 15 20

Arg Leu Ser Gln Cys Pro Asp Val Asp Pro Leu Ser Ile Pro Val
25 30 35

40 Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln
40 45 50

Thr Glu Gln Ser Lys Ala Gln Asp Ile Leu Gly Ala Val Ser Leu
55 60 65

45 Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Glu Pro Ser
70 75 80

Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu
85 90 95

50 Leu Leu Gly Ala Leu Gln Gly Leu Leu Gly Thr Gln Leu Pro Leu
100 105 110

	Gln Gly Arg Thr Thr	Ala His Lys Asp Pro	Asn Ala Leu Phe Leu
	115	120	125
5	Ser Leu Gln Gln Leu	Leu Arg Gly Lys Val	Arg Phe Leu Leu Leu
	130	135	140
	Val Glu Gly Pro Thr	Leu Cys Val Arg Arg	Thr Leu Pro Thr Thr
	145	150	155
10	Ala Val Pro Ser Ser	Thr Ser Gln Leu Leu	Thr Leu Asn Lys Phe
	160	165	170
	Pro Asn Arg Thr Ser	Gly Leu Leu Glu Thr	Asn Phe Ser Val Thr
	175	180	185
15	Ala Arg Thr Ala Gly	Pro Gly Leu Leu Ser	Arg Leu Gln Gly Phe
	190	195	200
	Arg Val Lys Ile Thr	Pro Gly Gln Leu Asn	Gln Thr Ser Arg Ser
20	205	210	215
	Pro Val Gln Ile Ser	Gly Tyr Leu Asn Arg	Thr His Gly Pro Val
	220	225	230
25	Asn Gly Thr His Gly	Leu Phe Ala Gly Thr	Ser Leu Gln Thr Leu
	235	240	245
	Glu Ala Ser Asp Ile	Ser Pro Gly Ala Phe	Asn Lys Gly Ser Leu
	250	255	260
30	Ala Phe Asn Leu Gln	Gly Gly Leu Pro Pro	Ser Pro Ser Leu Ala
	265	270	275
35	Pro Asp Gly His Thr	Pro Phe Pro Pro Ser	Pro Ala Leu Pro Thr
	280	285	290
	Thr His Gly Ser Pro	Pro Gln Leu His Pro	Leu Phe Pro Asp Pro
	295	300	305
40	Ser Thr Thr Met Pro	Asn Ser Thr Ala Pro	His Pro Val Thr Met
	310	315	320
45	Tyr Pro His Pro Arg	Asn Leu Ser Gln Glu	Thr
	325	330	335

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

	Ser	Pro	Val	Ala	Pro	Ala	Cys	Asp	Pro	Arg	Leu	Leu	Asn	Lys	Leu	
	1				5					10					15	
5	Leu	Arg	Asp	Ser	His	Leu	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro	
					20					25					30	
10	Asp	Val	Asp	Pro	Leu	Ser	Ile	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	
					35					40					45	
	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Thr	Glu	Gln	Ser	Lys	Ala	
					50					55					60	
15	Gln	Asp	Ile	Leu	Gly	Ala	Val	Ser	Leu	Leu	Leu	Glu	Gly	Val	Met	
					65					70					75	
	Ala	Ala	Arg	Gly	Gln	Leu	Glu	Pro	Ser	Cys	Leu	Ser	Ser	Leu	Leu	
					80					85					90	
20	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	
					95					100					105	
	Gly	Leu	Leu	Gly	Thr	Gln	Leu	Pro	Leu	Gln	Gly	Arg	Thr	Thr	Ala	
25					110					115					120	
	His	Lys	Asp	Pro	Asn	Ala	Leu	Phe	Leu	Ser	Leu	Gln	Gln	Leu	Leu	
					125					130					135	
30	Arg	Gly	Lys	Asp	Phe	Trp	Ile	Val	Gly	Asp	Glu	Leu	Gln	Cys	His	
					140					145					150	
	Ser	Gln	Asn	Cys	Trp	Pro	Trp	Thr	Ser	Glu	Gln	Ala	Ser	Gly	Ile	
					155					160					165	
35	Gln	Ser	Gln	Asp	Tyr	Ser	Trp	Ser	Ala	Lys	Ser	Asn	Leu	Gln	Val	
					170					175					180	
	Pro	Ser	Pro	Asn	Leu	Trp	Ile	Pro	Glu	Gln	Asp	Thr	Arg	Thr	Cys	
40					185					190					195	
	Glu	Trp	Asn	Ser	Trp	Ala	Leu	Cys	Trp	Asn	Leu	Thr	Ser	Asp	Pro	
					200					205					210	
45	Gly	Ser	Leu	Arg	His	Leu	Ala	Arg	Ser	Phe	Gln	Gln	Arg	Leu	Pro	
					215					220					225	
	Gly	Ile	Gln	Pro	Pro	Gly	Trp	Thr	Ser	Ser	Phe	Ser	Lys	Pro	Cys	
50					230					235					240	
	Ser															

(2) INFORMATION FOR SEQ ID NO:16:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 335 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser Pro Val Ala Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
 1 5 10 15
 Leu Arg Asp Ser His Leu Leu His Ser Arg Leu Ser Gln Cys Pro
 20 25 30
 Asp Val Asp Pro Leu Ser Ile Pro Val Leu Leu Pro Ala Val Asp
 35 40 45
 Phe Ser Leu Gly Glu Trp Lys Thr Gln Thr Glu Gln Ser Lys Ala
 50 55 60
 Gln Asp Ile Leu Gly Ala Val Ser Leu Leu Leu Glu Gly Val Met
 65 70 75
 Ala Ala Arg Gly Gln Leu Glu Pro Ser Cys Leu Ser Ser Leu Leu
 80 85 90
 Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln
 95 100 105
 Gly Leu Leu Gly Thr Gln Leu Pro Leu Gln Gly Arg Thr Thr Ala
 110 115 120
 His Lys Asp Pro Asn Ala Leu Phe Leu Ser Leu Gln Gln Leu Leu
 125 130 135
 Arg Gly Lys Val Arg Phe Leu Leu Leu Val Glu Gly Pro Thr Leu
 140 145 150
 Cys Val Arg Arg Thr Leu Pro Thr Thr Ala Val Pro Ser Ser Thr
 155 160 165
 Ser Gln Leu Leu Thr Leu Asn Lys Phe Pro Asn Arg Thr Ser Gly
 170 175 180
 Leu Leu Glu Thr Asn Phe Ser Val Thr Ala Arg Thr Ala Gly Pro
 185 190 195
 Gly Leu Leu Ser Arg Leu Gln Gly Phe Arg Val Lys Ile Thr Pro

200

205

210

Gly Gln Leu Asn Gln Thr Ser Arg Ser Pro Val Gln Ile Ser Gly
215 220 225

5

Tyr Leu Asn Arg Thr His Gly Pro Val Asn Gly Thr His Gly Leu
230 235 240

10

Phe Ala Gly Thr Ser Leu Gln Thr Leu Glu Ala Ser Asp Ile Ser
245 250 255

Pro Gly Ala Phe Asn Lys Gly Ser Leu Ala Phe Asn Leu Gln Gly
260 265 270

15

Gly Leu Pro Pro Ser Pro Ser Leu Ala Pro Asp Gly His Thr Pro
275 280 285

Phe Pro Pro Ser Pro Ala Leu Pro Thr Thr His Gly Ser Pro Pro
290 295 300

20

Gln Leu His Pro Leu Phe Pro Asp Pro Ser Thr Thr Met Pro Asn
305 310 315

25

Ser Thr Ala Pro His Pro Val Thr Met Tyr Pro His Pro Arg Asn
320 325 330

Leu Ser Gln Glu Thr
335

30

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

40

Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
1 5 10 15

Leu Arg Asp Ser His Val Leu His Gly Arg Leu Ser Gln Cys Pro
20 25 30

45

Asp Ile Asn Pro Leu Ser Thr Pro Val Leu Leu Pro Ala Val Asp
35 40 45

50

Phe Thr Leu Gly Glu Trp Lys Thr Gln Thr Glu Gln Thr Lys Ala
50 55 60

Gln Asp Val Leu Gly Ala Thr Thr Leu Leu Leu Glu Ala Val Met

65

70

75

Thr Ala Arg Gly Gln Val Gly Pro Pro Cys Leu Ser Ser Leu Leu
80 85 90

5

Val Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln
95 100 105

10

Asp Leu Leu Gly Met Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala
110 115 120

His Lys Asp Pro Ser Ala Ile Phe Leu Asn Phe Gln Gln Leu Leu
125 130 135

15

Arg Gly Lys Val Arg Phe Leu Leu Leu Val Val Gly Pro Ser Leu
140 145 150

Cys Ala Lys Arg Ala Pro Pro Ala Ile Ala Val Pro Ser Ser Thr
155 160 165

20

Ser Pro Phe His Thr Leu Asn Lys Leu Pro Asn Arg Thr Ser Gly
170 175 180

25

Leu Leu Glu Thr Asn Ser Ser Ile Ser Ala Arg Thr Thr Gly Ser
185 190 195

Gly Phe Leu Lys Arg Leu Gln Ala Phe Arg Ala Lys Ile Pro Gly
200 205 210

30

Leu Leu Asn Gln Thr Ser Arg Ser Leu Asp Gln Ile Pro Gly His
215 220 225

Gln Asn Gly Thr His Gly Pro Leu Ser Gly Ile His Gly Leu Phe
230 235 240

35

Pro Gly Pro Gln Pro Gly Ala Leu Gly Ala Pro Asp Ile Pro Pro
245 250 255

40

Ala Thr Ser Gly Met Gly Ser Arg Pro Thr Tyr Leu Gln Pro Gly
260 265 270

Glu Ser Pro Ser Pro Ala His Pro Ser Pro Gly Arg Tyr Thr Leu
275 280 285

45

Phe Ser Pro Ser Pro Thr Ser Pro Ser Pro Thr Val Gln Leu Gln
290 295 300

50

Pro Leu Leu Pro Asp Pro Ser Ala Ile Thr Pro Asn Ser Thr Ser
305 310 315

Pro Leu Leu Phe Ala Ala His Pro His Phe Gln Asn Leu Ser Gln

Glu Glu
332

5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 1026 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AGCCCGGCTC CTCCTGCCTG TGACCCCCGA CTCCTAAATA AACTGCTTCG 50

20

TGACTCCCAT GTCCTTCACG GCAGACTGAG CCAGTGCCCA GACATTAACC 100

CTTTGTCCAC ACCTGTCCTG CTGCCTGCTG TGGACTTCAC CTTGGGAGAA 150

25

TGGAAAACCC AGACGGAGCA GACAAAGGCA CAGGATGTCC TGGGAGCCAC 200

AACCCTTCTG CTGGAGGCAG TGATGACAGC ACGGGGACAA GTGGGACCCC 250

30

CTTGCCTCTC ATCCCTGCTG GTGCAGCTTT CTGGACAGGT TCGCCTCCTC 300

35

CTCGGGGCCC TGCAGGACCT CCTTGGAATG CAGCTTCCTC CACAGGGAAG 350

GACCACAGCT CACAAGGATC CCAGTGCCAT CTTCTGAAC TTCCAACAAC 400

40

TGCTCCGAGG AAAGGTGCGT TTCCTGCTCC TTGTAGTGGG GCCCTCCCTC 450

TGTGCCAAGA GGGCCCCACC CGCCATAGCT GTCCCGAGCA GCACCTCTCC 500

45

ATTCCACACA CTGAACAAGC TCCCAAACAG GACCTCTGGA TTGTTGGAGA 550

50

CAAACCTCCAG TATCTCAGCC AGAACTACTG GCTCTGGATT TCTCAAGAGG 600

CTGCAGGCAT TCAGAGCCAA GATTCCTGGT CTGCTGAACC AAACCTCCAG 650
 GTCCCTAGAC CAAATCCCTG GACACCAGAA TGGGACACAC GGACCCTTGA 700
 GTGGAATTCA TGGACTCTTT CCTGGACCCC AACCCGGGGC CCTCGGAGCT 750
 CCAGACATTC CTCCAGCAAC TTCAGGCATG GGCTCCCGGC CAACCTACCT 800
 CCAGCCTGGA GAGTCTCCTT CCCCAGCTCA CCCTTCTCCT GGACGATACA 850
 CTCTCTTCTC TCCTTCACCC ACCTCGCCCT CCCCCACAGT CCAGCTCCAG 900
 CCTCTGCTTC CTGACCCCTC TGCATCACA CCCAACTCTA CCAGTCCTCT 950
 TCTATTTGCA GCTCACCTC ATTTCCAGAA CCTGTCTCAG GAAGAGTAAG 1000
 GTGCTCAGAC CCTGCCAACT TCAGCA 1026

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1014 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGCCCGGCTC CTCCTGCCTG TGACCCCGA CTCCTAAATA AACTGCTTCG 50
 TGA CTCCAT GTCCTTCACG GCAGACTGAG CCAGTGCCCA GACATTAACC 100
 CTTTGTCCAC ACCTGTCCTG CTGCCTGCTG TGGACTTCAC CTTGGGAGAA 150
 TGGAAAACCC AGACGGAGCA GACAAAGGCA CAGGATGTCC TGGGAGCCAC 200
 AACCTTCTG CTGGAGGCAG TGATGACAGC ACGGGGACAA GTGGGACCCC 250

CTTGCCTCTC ATCCCTGCTG GTGCAGCTTT CTGGACAGGT TCGCCTCCTC 300

5 CTCGGGGCCC TGCAGGACCT CCTTGGAATG CAGGGAAGGA CCACAGCTCA 350

CAAGGATCCC AGTGCCATCT TCCTGAACTT CCAACAACCTG CTCCGAGGAA 400

10 AGGTGCGTTT CCTGCTCCTT GTAGTGGGGC CCTCCCTCTG TGCCAAGAGG 450

15 GCCCCACCCG CCATAGCTGT CCCGAGCAGC ACCTCTCCAT TCCACACACT 500

GAACAAGCTC CCAAACAGGA CCTCTGGATT GTTGGAGACA AACTCCAGTA 550

20 TCTCAGCCAG AACTACTGGC TCTGGATTTC TCAAGAGGCT GCAGGCATTC 600

AGAGCCAAGA TTCCTGGTCT GCTGAACCAA ACCTCCAGGT CCCTAGACCA 650

25 AATCCCTGGA CACCAGAATG GGACACACGG ACCCTTGAGT GGAATTCATG 700

30 GACTCTTTCC TGGACCCCAA CCCGGGGCCC TCGGAGCTCC AGACATTCTT 750

Point
CCAGCAACTT CAGGCATGGG CTCCCGGCCA ACCTACCTCC AGCCTGGAGA 800

35 GTCTCCTTCC CCAGCTCACC CTTCTCCTGG ACGATACTCT CTCTTCTCTC 850

CTTCACCCAC CTCGCCCTCC CCCACAGTCC AGCTCCAGCC TCTGCTTCCT 900

40 GACCCCTCTG CGATCACACC CAACTCTACC AGTCCTCTTC TATTTGCAGC 950

45 TCACCCTCAT TTCCAGAACC TGTCTCAGGA AGAGTAAGGT GCTCAGACCC 1000

TGCCAACTTC AGCA 1014

50 (2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 328 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

5	Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Pro	Arg	Leu	Leu	Asn	Lys	Leu	1	5	10	15
10	Leu	Arg	Asp	Ser	His	Val	Leu	His	Gly	Arg	Leu	Ser	Gln	Cys	Pro	20	25	30	
15	Asp	Ile	Asn	Pro	Leu	Ser	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	35	40	45	
	Phe	Thr	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Thr	Glu	Gln	Thr	Lys	Ala	50	55	60	
20	Gln	Asp	Val	Leu	Gly	Ala	Thr	Thr	Leu	Leu	Leu	Glu	Ala	Val	Met	65	70	75	
	Thr	Ala	Arg	Gly	Gln	Val	Gly	Pro	Pro	Cys	Leu	Ser	Ser	Leu	Leu	80	85	90	
25	Val	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	95	100	105	
30	Asp	Leu	Leu	Gly	Met	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	110	115	120	
<i>B1 cont</i>	Ser	Ala	Ile	Phe	Leu	Asn	Phe	Gln	Gln	Leu	Leu	Arg	Gly	Lys	Val	125	130	135	
35	Arg	Phe	Leu	Leu	Leu	Val	Val	Gly	Pro	Ser	Leu	Cys	Ala	Lys	Arg	140	145	150	
	Ala	Pro	Pro	Ala	Ile	Ala	Val	Pro	Ser	Ser	Thr	Ser	Pro	Phe	His	155	160	165	
40	Thr	Leu	Asn	Lys	Leu	Pro	Asn	Arg	Thr	Ser	Gly	Leu	Leu	Glu	Thr	170	175	180	
45	Asn	Ser	Ser	Ile	Ser	Ala	Arg	Thr	Thr	Gly	Ser	Gly	Phe	Leu	Lys	185	190	195	
	Arg	Leu	Gln	Ala	Phe	Arg	Ala	Lys	Ile	Pro	Gly	Leu	Leu	Asn	Gln	200	205	210	
50	Thr	Ser	Arg	Ser	Leu	Asp	Gln	Ile	Pro	Gly	His	Gln	Asn	Gly	Thr	215	220	225	

His Gly Pro Leu Ser Gly Ile His Gly Leu Phe Pro Gly Pro Gln
230 235 240

5 Pro Gly Ala Leu Gly Ala Pro Asp Ile Pro Pro Ala Thr Ser Gly
245 250 255

Met Gly Ser Arg Pro Thr Tyr Leu Gln Pro Gly Glu Ser Pro Ser
260 265 270

10 Pro Ala His Pro Ser Pro Gly Arg Tyr Thr Leu Phe Ser Pro Ser
275 280 285

Pro Thr Ser Pro Ser Pro Thr Val Gln Leu Gln Pro Leu Leu Pro
290 295 300

15 Asp Pro Ser Ala Ile Thr Pro Asn Ser Thr Ser Pro Leu Leu Phe
305 310 315

20 Ala Ala His Pro His Phe Gln Asn Leu Ser Gln Glu Glu
320 325 328

(2) INFORMATION FOR SEQ ID NO:21:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

30 Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
1 5 10 15

Cont
35 Leu Arg Asp Asp His Val Leu His Gly Arg
20 25

(2) INFORMATION FOR SEQ ID NO:22:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

45 Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
1 5 10 15

50 Leu Arg Asp Asp His Ser Val Leu His Gly Arg Leu
20 25 27

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Ser Pro Ala Pro Pro Ala Xaa Asp Pro Arg Leu Leu Asn Lys Leu
1 5 10 15
Leu Arg Asp Asp His Val Leu His Gly Arg
20 25

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Xaa Pro Ala Pro Pro Ala Xaa Asp Pro Arg Leu Xaa Asn Lys
1 5 10 14

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Pro Arg Leu Leu Asn Lys Leu Leu Arg
1 5 9

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCCGTGAAGG ACGTGGTCGT CACGAAGCAG TTTATTTAGG AGTCG 45

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCNGCNCNCNC CNGCNTGYGA 20

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

NCCRTGNARN ACRTGRTCRT C 21

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCAGCGCCGC CAGCCTGTGA CCCCCGACTC CTAAATAAAC TGCCTCGTGA 50

TGACCACGTT CAGCACGGC 69

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GCCGTGCTGA ACGTGGTCAT CACGAGGCAG TTTATTTAGG AGTCGGGGGT 50

10

CACAGGCTGG CGGCGCTGG 69

15 (2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 69 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

25

CCAGCACCTC CGGCATGTGA CCCCCGACTC CTAAATAAAC TGCTTCGTGA 50

30

CGACCACGTC CATCACGGC 69

B1 cont
35 (2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 69 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

45 GCCGTGATGG ACGTGGTCGT CACGAAGCAG TTTATTTAGG AGTCGGGGGT 50

50

CACATGCCGG AGGTGCTGG 69

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CCAGCACCGC CGGCATGTGA CCCCCGACTC CTAAATAAAC TGCTTCGTGA 50
CGATCATGTC TATCACGGT 69

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ACCGTGATAG ACATGATCGT CACGAAGCAG TTTATTTAGG AGTCGGGGGT 50
CACATGCCGG CGGTGCTGG 69

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GCTAGCTCTA GAAATTGCTC CTCGTGGTCA TGCTTCT 37

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CAGTCTGCCG TGAAGGACAT GG 22

10

(2) INFORMATION FOR SEQ ID NO:37:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TGTGGACTTT AGCTTGGGAG AATG 24

25

(2) INFORMATION FOR SEQ ID NO:38:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GGTCCAGGGA CCTGGAGGTT TG 22

40

(2) INFORMATION FOR SEQ ID NO:39:

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ATCGATATCG ATAGCCAGAC ACCCCGGCCA G 31

5 (2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GCTAGCTCTA GACAGGGAAG GGAGCTGTAC ATGAGA 36

20 (2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTCCTTGGA CCCAGGGCAG GACC 24

35 (2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GGTCCTGCCC TGGGTTCCAA GGAG 24

50 (2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTGCTCCGAG GAAAGGACTT CTGGATT 27

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

AATCCAGAAG TCCTTTCCTC GGAGCAG 27

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CCCTCTGCGT CGCGGCGGCC CCACCCAC 28

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GTGGGTGGGG CCGCCGCGAC GCAGAGGG 28

5 (2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GACTCGAGGA TCCATCGATT TTTTTTTTTT TTTT 35

20 (2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GACTCGAGGA TCCATCG 17

35 (2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GCTAGCTCTA GAAGCCCGGC TCCTCCTGCC TG 32

50 (2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CGAAATTAAC CCTCACTAAA G 21

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

His Val Leu His
1 4

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Ser Arg Leu Ser
1 4

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Ser His Val Leu
1 4

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

His Ser Arg Leu
1 4

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala Val Asp Phe
1 4

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ser Leu Gly Glu
1 4

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Ala Val Thr Leu
1 4

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Leu Leu Glu Gly
1 4

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Leu Ser Ser Leu
1 4

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Leu Gly Gln Leu
1 4

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Cys Leu Ser Ser
1 4

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Leu Leu Gly Gln
1 4

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ser Ser Leu Leu
1 4

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Gly Gln Leu Ser
1 4

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Leu Gln Ser Leu
1 4

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Leu Gly Thr Gln
1 4

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Ala Leu Gln Ser
1 4

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Leu Leu Gly Thr
1 4

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Asn Ala Ile Phe
1 4

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Leu Ser Phe Gln
1 4

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu
1 5 10 15

Leu Arg Asp Ser His Val Leu
20 22

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

His Ser Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr
1 5 10 15
Pro Val Leu Leu Pro Ala Val Asp Phe
20 24

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln
1 5 10 15
Asp Ile Leu Gly Ala Val Thr Leu
20 23

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr
1 5 10 15
Cys Leu Ser Ser Leu Leu
20 21

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

5 Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln
1 5 10 15

10 Ser
16

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

20 Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His
1 5 10 15

25 Lys Asp Pro Asn Ala Ile Phe
20 22

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

35 Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met
1 5 10 15

40 Leu Val Gly Gly Ser Thr Leu Cys Val Arg
20 25